FIGURE 1

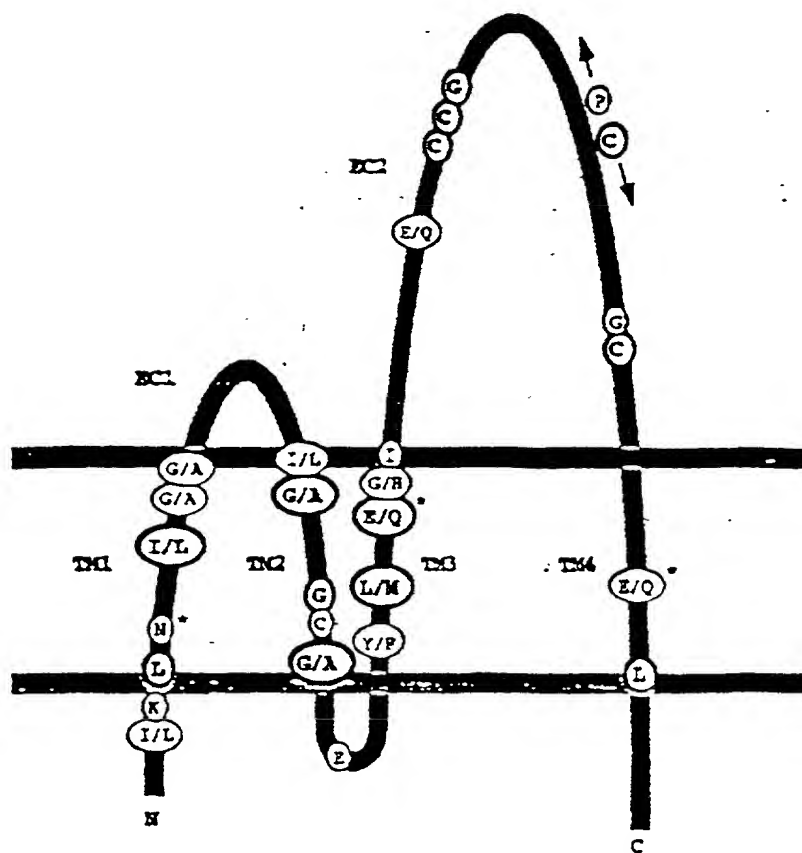# FIGURE 2A

```
  1    CTTCCTCGGC CGAGCCGGGC CGCGCGGCCG CTGCCGCCGC CGCGCGCGGA
       GAAGGAGCCG GCTCGGCCCG GCGCGCCGGC GACGGCGGCG GCGCGCGCCT
```

```
 +1                 ]------------------------------------
 51    TTCTGCTTCT CAGAAGATGC ACTATTATAG ATACTCTAAC GCCAAGGTCA
       AAGACGAAGA GTCTTCTACG TGATAATATC TATGAGATTG CGGTTCCAGT
```

```
 +1    -----------------------------------------------------
101    GCTGCTGGTA CAAGTACCTC CTTTTCAGCT ACAACATCAT CTTCTGGTTG
       CGACGACCAT GTTCATGGAG GAAAAGTCGA TGTTGTAGTA GAAGACCAAC
 -3                                       <------------------
```

```
 +3                             ]----------------------
 +1    -----------------------------------------------------
151    GCTGGAGTTG TCTTCCTTGG AGTCGGGCTG TGGGCATGGA GCGAAAAGGG
       CGACCTCAAC AGAAGGAACC TCAGCCCGAC ACCCGTACCT CGCTTTTCCC
 -3    -----------------------------------------------------
```

```
 +3    -----------------------------------------------------
 +1    -----------------------------------------------------
201    TGTGCTGTCC GACCTCACCA AAGTGACCCG GATGCATGGA ATCGACCCTG
       ACACGACAGG CTGGAGTGGT TTCACTGGGC CTACGTACCT TAGCTGGGAC
 -3    -----------------------------------------------------
```

```
 +3    -----------------------------------------------------
 +1    -----------------------------------------------------
251    TGGTGCTGGT CCTGATGGTG GGCGTGGTGA TGTTCACCCT GGGGTTCGCC
       ACCACGACCA GGACTACCAC CCGCACCACT ACAAGTGGGA CCCCAAGCGG
 -3    -----------------------------------------------------
```

```
 +3    -----------------------------------------------------
 +1    -----------------------------------------------------
301    GGCTGCGTGG GGGCTCTGCG GGAGAATATC TGCTTGCTCA ACTTTTTCTG
       CCGACGCACC CCCGAGACGC CCTCTTATAG ACGAACGAGT TGAAAAAGAC
 -3    -----------------------------------------------------
```

```
 +3    -----------------------------------------------------
 +1    -----------------------------------------------------
351    TGGCACCATC GTGCTCATCT TCTTCCTGGA GCTGGCTGTG GCCGTGCTGG
       ACCGTGGTAG CACGAGTAGA AGAAGGACCT CGACCGACAC CGGCACGACC
 -3    -----------------------------------------------------
```

```
 +3    -----------------------------------------------------
 +1    -----------------------------------------------------
401    CCTTCCTGTT CCAGGACTGG GTGAGGGACC GGTTCCGGGA GTTCTTCGAG
       GGAAGGACAA GGTCCTGACC CACTCCCTGG CCAAGGCCCT CAAGAAGCTC
 -3    -----------------------------------------------------
```

```
 +3    -----------------------------------------------------
 +1    -----------------------------------------------------
                             ClaI
                          ~~~~~~~
451    AGCAACATCA AGTCCTACCG GGACGATATC GATCTGCAAA ACCTCATCGA
       TCGTTGTAGT TCAGGATGGC CCTGCTATAG CTAGACGTTT TGGAGTAGCT
 -3    -------[
```

```
 +3    ---------------->
 +1    -----------------------------------------------------
501    CTCCCTTCAG AAAGCTAACC AGTGCTGTGG CGCATATGGC CCTGAAGACT
       GAGGGAAGTC TTTCGATTGG TCACGACACC GCGTATACCG GGACTTCTGA
```

FIGURE 2B

```
      +1  -----------------------------------------------
    551   GGGACCTCAA CGTCTACTTC AATTGCAGCG GTGCCAGCTA CAGCCGAGAG
          CCCTGGAGTT GCAGATGAAG TTAACGTCGC CACGGTCGAT GTCGGCTCTC


      +1  -----------------------------------------------
    601   AAGTGCGGGG TCCCCTTCTC CTGCTGCGTG CCAGATCCTG CGCAAAAAGT
          TTCACGCCCC AGGGGAAGAG GACGACGCAC GGTCTAGGAC GCGTTTTTCA


      +1  -----------------------------------------------
    651   TGTGAACACA CAGTGTGGAT ATGATGTCAG GATTCAGCTG AAGAGCAAGT
          ACACTTGTGT GTCACACCTA TACTACAGTC CTAAGTCGAC TTCTCGTTCA


      +1  -----------------------------------------------
    701   GGGATGAGTC CATCTTCACG AAAGGCTGCA TCCAGGCGCT GGAAAGCTGG
          CCCTACTCAG GTAGAAGTGC TTTCCGACGT AGGTCCGCGA CCTTTCGACC


      +1  -----------------------------------------------
    751   CTCCCGCGGA ACATTTACAT TGTGGCTGGC GTCTTCATCG CCATCTCGCT
          GAGGGCGCCT TGTAAATGTA ACACCGACCG CAGAAGTAGC GGTAGAGCGA
      -1                                      <-------------


      +1  -----------------------------------------------
    801   GTTGCAGATA TTTGGCATCT TCCTGGCAAG GACGCTGATC TCAGACATCG
          CAACGTCTAT AAACCGTAGA AGGACCGTTC CTGCGACTAG AGTCTGTAGC
      -1  -----------------------------------------------


      +1  -------------------------->
    851   AGGCAGTGAA GGCCGGCCAT CACTTCTGAG GAGCAGAGTT GAGGGAGCCG
          TCCGTCACTT CCGGCCGGTA GTGAAGACTC CTCGTCTCAA CTCCCTCGGC
      -1  -----------------------------------------------


    901   AGCTGAGCCA CGCTGGGAGG CCAGAGCCTT TCTCTGCCAT CAGCCCTACG
          TCGACTCGGT GCGACCCTCC GGTCTCGGAA AGAGACGGTA GTCGGGATGC
      -1  -----------------------------------------------


      +1                              ]-----------------
    951   TCCAGAGGGA GAGGAGCCGA CACCCCCAGA GCCAGTGCCC CATCTTAAGC
          AGGTCTCCCT CTCCTCGGCT GTGGGGGTCT CGGTCACGGG GTAGAATTCG
      -1  -----------------------[


      +1  -----------------------------------------------
   1001   ATCAGCGTGA CGTGACCTCT CTGTTTCTGC TTGCTGGTGC TGAAGACCAA
          TAGTCGCACT GCACTGGAGA GACAAAGACG AACGACCACG ACTTCTGGTT


      +1  -----------------------------------------------
   1051   GGGTCCCCCT TGTTACCTGC CCAAACTTGT GACTGCATCC CTCTGGAGTC
          CCCAGGGGGA ACAATGGACG GGTTTGAACA CTGACGTAGG GAGACCTCAG


      +1  -----------------------------------------------
   1101   TACCCAGAGA CAGAGAATGT GTCTTTATGT GGGAGTNGTG ACTCTGAAAG
          ATGGGTCTCT GTCTCTTACA CAGAAATACA CCCTCANCAC TGAGACTTTC
      -1     <--------------------------------------------


      +1  -----------------------------------------------
                                              PstI
                                              ~~~~
   1151   ACAGAGAGGG CTCCTGTGGS TGCCAGGAGG GCTTGACTCA GACCCCCTGC
          TGTCTCTCCC GAGGACACCS ACGGTCCTCC CGAACTGAGT CTGGGGGACG
      -1  -----------------------------------------------
```

FIGURE 2C

```
  +1  --------------------------------------------------------
       PstI
       ~~
1201  AGCTCAAGCA TGTYTGCAGG ACACCCTGGT CCCYTYTCCA YTGGCWTCCA
      TCGAGTTCGT ACARACGTCC TGTGGGACCA GGGRARAGGT RACCGWAGGT
  -1  --------------------------------------------------------


  +1  ----------------------------------------------->
1251  GACATCTGCT TTGGGTCATC CACATCTGTG GGTNGGCCGT GGGTAGAGGG
      CTGTAGACGA AACCCAGTAG GTGTAGACAC CCANCCGGCA CCCATCTCCC
  -1  --------------------------------------------------------


1301  ACCCACAGGC GTGGACAGGG CATCTCTCTC CATCAAGCAA AGCAGCATGG
      TGGGTGTCCG CACCTGTCCC GTAGAGAGAG GTAGTTCGTT TCGTCGTACC
  -1  -------------------------------------------------[


1351  GGGGCCTTGC CGTAAACGGG AGGCGNGACG TTGGCCC
      CCCCGGAACG GCATTTGCCC TCCGCNCTGC AACCGGG
```

FIGURE 3

```
  1   MHYYRYSNAK VSCWYKYLLF SYNIIFWLAG VVFLGVGLWA WSEKGVLSDL

 51   TKVTRMHGID PVVLVLMVGV VMFTLGFAGC VGALRENICL LNFFCGTIVL

101   IFFLELAVAV LAFLFQDWVR DRFREFFESN IKSYRDDIDL QNLIDSLQKA

151   NQCCGAYGPE DWDLNVYFNC SGASYSREKC GVPFSCCVPD PAQKVVNTQC

201   GYDVRIQLKS KWDESIFTKG CIQALESWLP RNIYIVAGVF IAISLLQIFG

251   IFLARTLISD IEAVKAGHHF
```

FIGURE 4

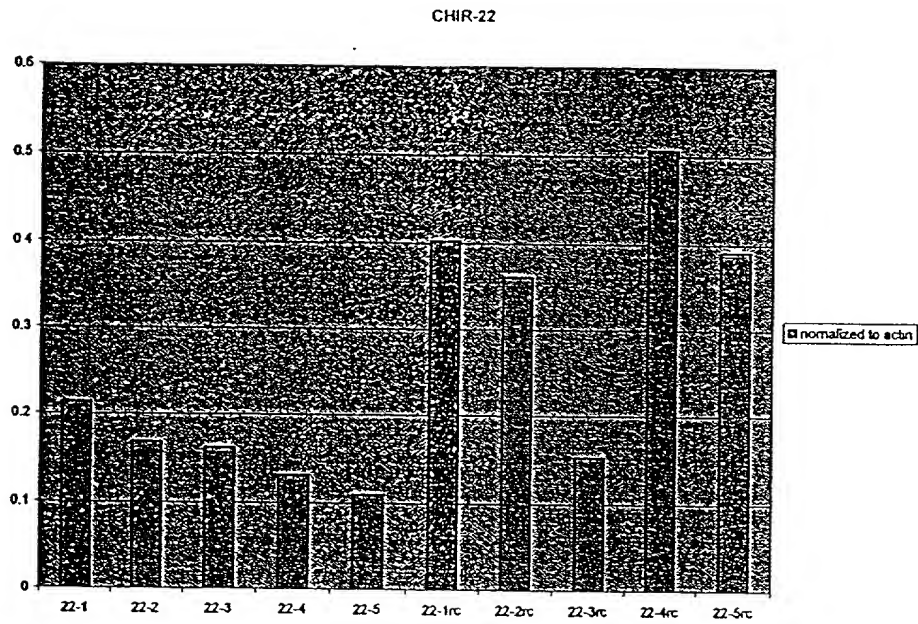| NTSP5:P104 | CHIR22-1 | TGCAGCCTTTCGTGAAGATGGACTC | 25 (7-11-7) |
NTSP5:P727	CHIR22-2	CCCCATGCTGCTTTGCTTGATGGAG	25 (7-11-7)
NTSP5:P285	CHIR22-3	GCTCAGCTCGGCTCCCTCAACTC	23 (7-9-7)
NTSP5:P456	CHIR22-4	CACAAGTTTGGGCAGGTAACAAGGG	25 (7-11-7)
NTSP5:P395	CHIR22-5	AGAGGTCACGTCACGCTGATGCTTA	25 (7-11-7)
NTSP5:P104	CHIR22-1RC	CTCAGGTAGAAGTGCTTTCCGACGT	25 (7-11-7)
NTSP5:P727	CHIR22-2RC	GAGGTAGTTCGTTTCGTCGTACCCC	25 (7-11-7)
NTSP5:P285	CHIR22-3RC	CTCAACTCCCTCGGCTCGACTCG	23 (7-9-7)
NTSP5:P456	CHIR22-4RC	GGGAACAATGGACGGGTTTGAACAC	25 (7-11-7)
NTSP5:P395	CHIR22-5RC	ATTCGTAGTCGCACTACGCTGGAGA	25 (7-11-7)

FIGURE 5

CHIR-22

FIGURE 6

Effect of NTSP5 AS on Growth of SW620